What is claimed is:

1. An isolated 80090, 52874, 52880, 63497, or 33425 nucleic acid molecule selected from the group consisting of:

a) a nucleic acid molecule comprising a nucleotide sequence which is at least 60% identical to the nucleotide sequence of SEQ ID NO:1,3,4,6,7,9,10,12,13 or 15, or the nucleotide sequence of the DNA insert of the plasmid deposited with ATCC as Accession Number _____;

b) a nucleic acid molecule comprising a fragment of at least 15 nucleotides of the nucleotide sequence of SEQ ID NO:1,3,4,6,7,9,10,12,13 or 15, or the nucleotide sequence of the DNA insert of the plasmid deposited with ATCC as Accession Number _____;

c) a nucleic acid molecule which encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:2,5,8,11 or 14, or the amino acid sequence encoded by the cDNA insert of the plasmid deposited with the ATCC as Accession Number _____;

d) a nucleic acid molecule which encodes a fragment of a polypeptide comprising the amino acid sequence of SEQ ID NO:2,5,8,11 or 14, or the amino acid sequence encoded by the cDNA insert of the plasmid deposited with the ATCC as Accession Number _____, wherein the fragment comprises at least 15 contiguous amino acids of SEQ ID NO:2,5,8,11 or 14, or the amino acid sequence encoded by the cDNA insert of the plasmid deposited with the ATCC as Accession Number _____;

e) a nucleic acid molecule which encodes a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO:2,5,8,11 or 14, or the amino acid sequence encoded by the cDNA insert of the plasmid deposited with the ATCC as Accession Number _____, wherein the nucleic acid molecule hybridizes to a nucleic acid molecule comprising SEQ ID NO:1,3,4,6,7,9,10,12,13 or 15, or a complement thereof, under stringent conditions;

f) a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1,3,4,6,7,9,10,12,13 or 15, or the nucleotide sequence of the DNA insert of the plasmid deposited with ATCC as Accession Number _____; and

g) a nucleic acid molecule which encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:2,5,8,11 or 14, or the amino acid sequence encoded by the cDNA insert of the plasmid deposited with the ATCC as Accession Number _____.

2. The isolated nucleic acid molecule of claim 1, which is the nucleotide sequence SEQ ID NO:1,4,7,10 or 13.

3. A host cell which contains the nucleic acid molecule of claim 1.

4. An isolated 80090, 52874, 52880, 63497, or 33425 polypeptide selected from the group consisting of:

a) a polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 60% identical to a nucleic acid comprising the nucleotide sequence of SEQ ID NO:1,3,4,6,7,9,10,12,13 or 15, or the nucleotide sequence of the DNA insert of the plasmid deposited with ATCC as Accession Number _____, or a complement thereof;

b) a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO:2,5,8,11 or 14, or the amino acid sequence encoded by the cDNA insert of the plasmid deposited with the ATCC as Accession Number _____, wherein the polypeptide is encoded by a nucleic acid molecule which hybridizes to a nucleic acid molecule comprising SEQ ID NO:1,3,4,6,7,9,10,12,13 or 15, or a complement thereof under stringent conditions;

c) a fragment of a polypeptide comprising the amino acid sequence of SEQ ID NO:2,5,8,11 or 14, or the amino acid sequence encoded by the cDNA insert of the plasmid deposited with the ATCC as Accession Number _____, wherein the fragment comprises at least 15 contiguous amino acids of SEQ ID NO:2,5,8,11 or 14; and

d) the amino acid sequence of SEQ ID NO:2,5,8,11 or 14.

5. An antibody which selectively binds to a polypeptide of claim 4.

6. A method for producing a polypeptide selected from the group consisting of:

a) a polypeptide comprising the amino acid sequence of SEQ ID NO:2,5,8,11 or 14, or the amino acid sequence encoded by the cDNA insert of the plasmid deposited with the ATCC as Accession Number _____;

b) a polypeptide comprising a fragment of the amino acid sequence of SEQ ID NO:2,5,8,11 or 14, or the amino acid sequence encoded by the cDNA insert of the plasmid deposited with the ATCC as Accession Number _____, wherein the fragment comprises at least 15 contiguous amino acids of SEQ ID NO:2,5,8,11 or 14, or the amino acid sequence encoded by the cDNA insert of the plasmid deposited with the ATCC as Accession Number _____;

c) a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO:2,5,8,11 or 14, or the amino acid sequence encoded by the cDNA insert of the plasmid deposited with the ATCC as Accession Number _____, wherein the polypeptide is encoded by a nucleic acid molecule which hybridizes to a nucleic acid molecule comprising SEQ ID NO:1,3,4,6,7,9,10,12,13 or 15; and

d) the amino acid sequence of SEQ ID NO:2,5,8,11 or 14;

comprising culturing the host cell of claim 3 under conditions in which the nucleic acid molecule is expressed.

7. A method for detecting the presence of a nucleic acid molecule of claim 1 or a polypeptide encoded by the nucleic acid molecule in a sample, comprising:

a) contacting the sample with a compound which selectively hybridizes to the nucleic acid molecule of claim 1 or binds to the polypeptide encoded by the nucleic acid molecule; and

b) determining whether the compound hybridizes to the nucleic acid or binds to the polypeptide in the sample.

8. A kit comprising a compound which selectively hybridizes to a nucleic acid molecule of claim 1 or binds to a polypeptide encoded by the nucleic acid molecule and instructions for use.

9. A method for identifying a compound which binds to a polypeptide or modulates the activity of the polypeptide of claim 4 comprising the steps of:

a) contacting a polypeptide, or a cell expressing a polypeptide of claim 4 with a test compound; and

b) determining whether the polypeptide binds to the test compound or determining the effect of the test compound on the activity of the polypeptide.

10. A method for modulating the activity of a polypeptide of claim 4 comprising contacting the polypeptide or a cell expressing the polypeptide with a compound which binds to the polypeptide in a sufficient concentration to modulate the activity of the polypeptide.

11. A method of identifying a nucleic acid molecule associated with a disorder comprising:

a) contacting a sample from a subject with or at risk of developing a disorder comprising nucleic acid molecules with a hybridization probe comprising at least 25 contiguous nucleotides of SEQ ID NO:1,4,7,10 or 13 defined in claim 2; and

b) detecting the presence of a nucleic acid molecule in the sample that hybridizes to the probe, thereby identifying a nucleic acid molecule associated with a disorder.

12. A method of identifying a nucleic acid associated with a disorder comprising:

a) contacting a sample from a subject having a disorder or at risk of developing a disorder comprising nucleic acid molecules with a first and a second amplification primer, the first primer comprising at least 25 contiguous nucleotides of SEQ ID NO:1,4,7,10 or 13 defined in claim 2 and the second primer comprising at least 25 contiguous nucleotides from the complement of SEQ ID NO:1,4,7,10 or 13;

b) incubating the sample under conditions that allow nucleic acid amplification; and

c) detecting the presence of a nucleic acid molecule in the sample that is amplified, thereby identifying the nucleic acid molecule associated with a disorder.

13. A method of identifying a polypeptide associated with a disorder comprising:

a) contacting a sample comprising polypeptides with a 80090, 52874, 52880, 63497, or 33425 binding partner of the 80090, 52874, 52880, 63497, or 33425 polypeptide defined in claim 4; and

b) detecting the presence of a polypeptide in the sample that binds to the 80090, 52874, 52880, 63497, or 33425 binding partner, thereby identifying the polypeptide associated with a disorder.

14. A method of identifying a subject having a disorder or at risk for developing a disorder comprising:

a) contacting a sample obtained from the subject comprising nucleic acid molecules with a hybridization probe comprising at least 25 contiguous nucleotides of SEQ ID NO:1,4,7,10 or 13 defined in claim 2; and

b) detecting the presence of a nucleic acid molecule in the sample that hybridizes to the probe, thereby identifying a subject having a disorder or at risk for developing a disorder.

15. A method of identifying a subject having a disorder or at risk for developing a disorder comprising:

a) contacting a sample obtained from the subject comprising nucleic acid molecules with a first and a second amplification primer, the first primer comprising at least 25 contiguous nucleotides of SEQ ID NO:1,4,7,10 or 13 defined in claim 2 and the second primer comprising at least 25 contiguous nucleotides from the complement of SEQ ID NO:1,4,7,10 or 13;

b) incubating the sample under conditions that allow nucleic acid amplification; and

c) detecting the presence of a nucleic acid molecule in the sample that is amplified, thereby identifying a subject having a disorder or at risk for developing a disorder.

16. A method of identifying a subject having a disorder or at risk for developing a disorder comprising:

a) contacting a sample obtained from the subject comprising polypeptides with a 80090, 52874, 52880, 63497, or 33425 binding partner of the 80090, 52874, 52880, 63497, or 33425 polypeptide defined in claim 4; and

b) detecting the presence of a polypeptide in the sample that binds to the 80090, 52874, 52880, 63497, or 33425 binding partner, thereby identifying a subject having a disorder or at risk for developing a disorder.

17. A method for identifying a compound capable of treating a disorder characterized by aberrant 80090, 52874, 52880, 63497, or 33425 nucleic acid expression or 80090, 52874, 52880, 63497, or 33425 polypeptide activity comprising assaying the ability of the compound to modulate 80090, 52874, 52880, 63497, or 33425 nucleic acid expression or 80090, 52874, 52880, 63497, or 33425 polypeptide activity, thereby identifying a compound capable of treating a disorder characterized by aberrant 80090, 52874, 52880, 63497, or 33425 nucleic acid expression or 80090, 52874, 52880, 63497, or 33425 polypeptide activity.

18. A method for treating a subject having a disorder or at risk of developing a disorder comprising administering to the subject a 80090, 52874, 52880, 63497, or 33425 modulator of the nucleic acid molecule defined in claim 1 or the polypeptide encoded by the nucleic acid molecule or contacting a cell with a 80090, 52874, 52880, 63497, or 33425 modulator.

19. The method of claim 18, wherein the 80090, 52874, 52880, 63497, or 33425 modulator is

a) a small molecule;

b) peptide;

c) phosphopeptide;

d) anti-80090, 52874, 52880, 63497, or 33425 antibody;

e) a 80090, 52874, 52880, 63497, or 33425 polypeptide comprising the amino acid sequence of SEQ ID NO:2,5,8,11 or 14, or a fragment thereof;

f) a 80090, 52874, 52880, 63497, or 33425 polypeptide comprising an amino acid sequence which is at least 90 percent identical to the amino acid sequence of SEQ ID NO:2,5,8,11 or 14, wherein the percent identity is calculated using the ALIGN program for

comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4; or

g) an isolated naturally occurring allelic variant of a polypeptide consisting of the amino acid sequence of SEQ ID NO:2,5,8,11 or 14, wherein the polypeptide is encoded by a nucleic acid molecule which hybridizes to a complement of a nucleic acid molecule consisting of SEQ ID NO:1,4,7,10 or 13 at 6X SSC at 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 65°C.

20. The method of claim 18, wherein the 80090, 52874, 52880, 63497, or 33425 modulator is

a) an antisense 80090, 52874, 52880, 63497, or 33425 nucleic acid molecule;

b) is a ribozyme;

c) the nucleotide sequence of SEQ ID NO:1,4,7,10 or 13, or a fragment thereof;

d) a nucleic acid molecule encoding a polypeptide comprising an amino acid sequence which is at least 90 percent identical to the amino acid sequence of SEQ ID NO:2,5,8,11 or 14, wherein the percent identity is calculated using the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4;

e) a nucleic acid molecule encoding a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO:2,5,8,11 or 14, wherein the nucleic acid molecule which hybridizes to a complement of a nucleic acid molecule consisting of SEQ ID NO:1 at 6X SSC at 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 65°C; or

f) a gene therapy vector.

21. A method for evaluating the efficacy of a treatment of a disorder, in a subject, comprising:

treating a subject with a protocol under evaluation;

assessing the expression level of a 80090, 52874, 52880, 63497, or 33425 nucleic acid molecule defined in claim 1 or 80090, 52874, 52880, 63497, or 33425 polypeptide encoded by the 80090, 52874, 52880, 63497, or 33425 nucleic acid molecule,

wherein a change in the expression level of 80090, 52874, 52880, 63497, or 33425 nucleic acid or 80090, 52874, 52880, 63497, or 33425 polypeptide after the treatment, relative to the level before the treatment, is indicative of the efficacy of the treatment of a disorder.

22. A method of diagnosing a disorder in a subject, comprising:
evaluating the expression or activity of a 80090, 52874, 52880, 63497, or 33425 nucleic acid molecule defined in claim 1 or a 80090, 52874, 52880, 63497, or 33425 polypeptide encoded by the 80090, 52874, 52880, 63497, or 33425 nucleic acid molecule, such that a difference in the level of 80090, 52874, 52880, 63497, or 33425 nucleic acid or 80090, 52874, 52880, 63497, or 33425 polypeptide relative to a normal subject or a cohort of normal subjects is indicative of a disorder.

23. The method defined in claim 18, wherein the disorder is cancer or aberrant cellular proliferation and/or differentiation, heart disorders, cardiovascular disorders, including endothelial cell disorders, hematopoietic disorders, blood vessel disorders, brain disorders, pain and metabolic disorders, liver disorders and platelet disorders.

24. The method defined in claim 23, wherein the cancer or aberrant cellular proliferation and/or differentiation is breast, ovarian, prostate, colon, or lung cancer.